

SURFACE-MEDIATED ACTIVATION OF BLOOD COAGULATION (INTRINSIC SYSTEM)

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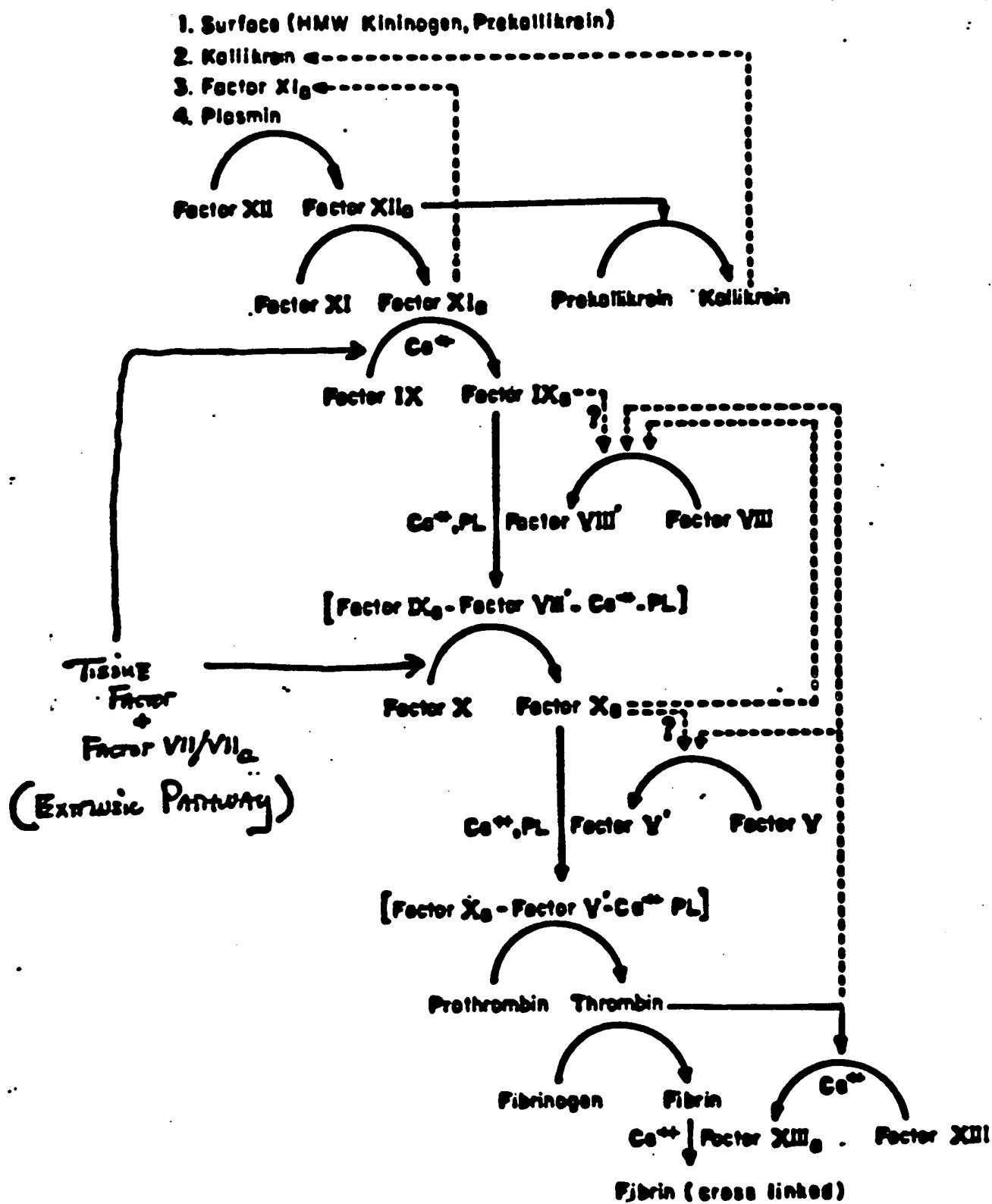
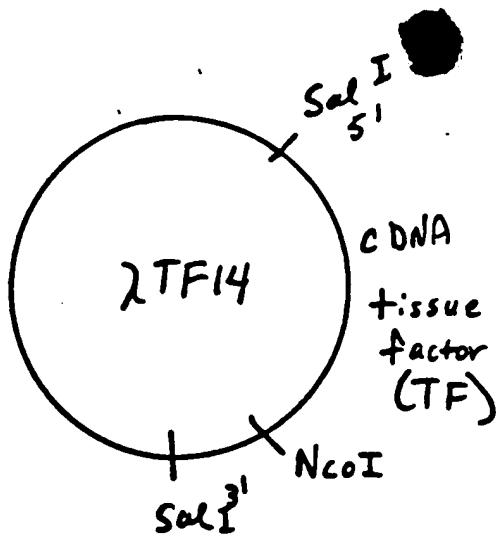
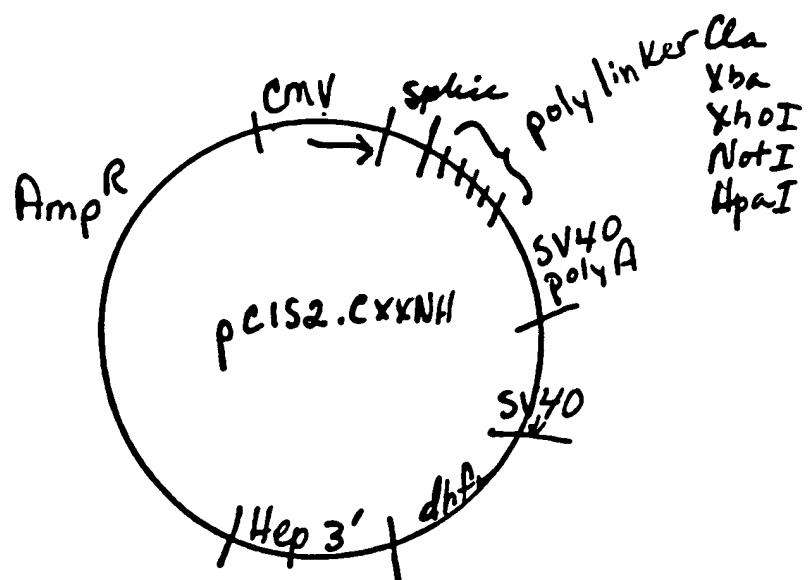


FIGURE 1

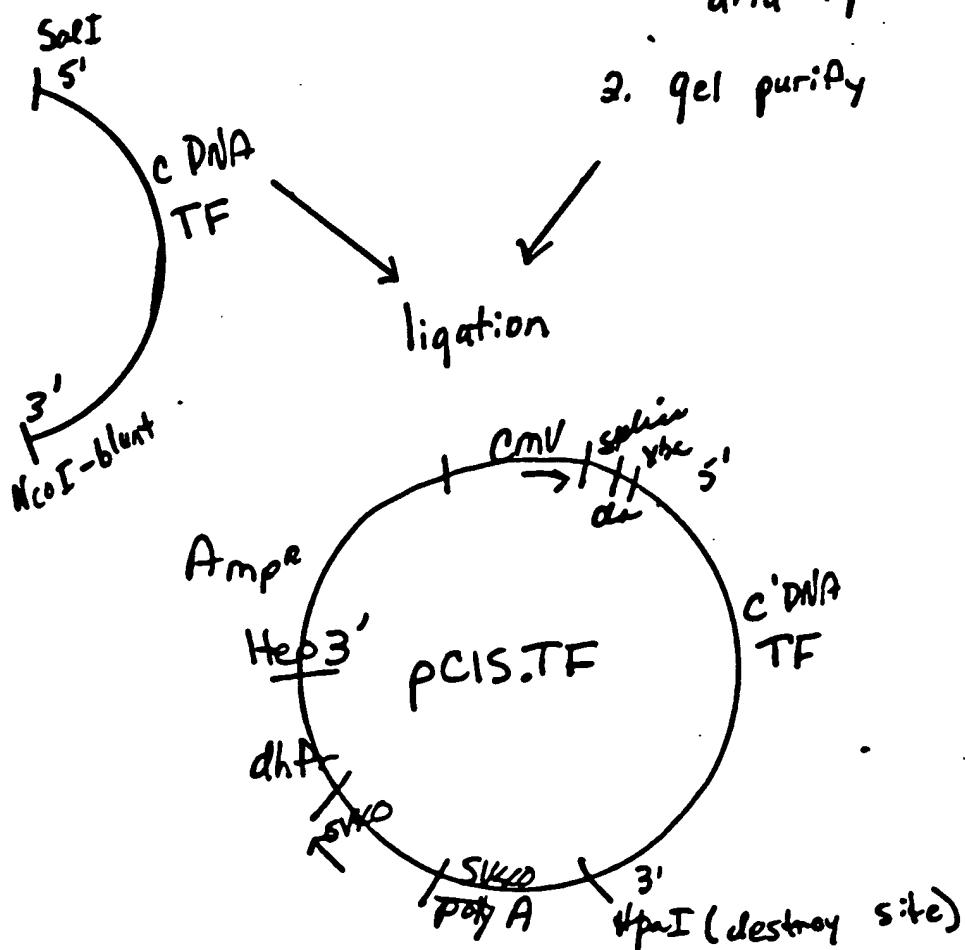
FIGURE 4



1. cut with NcoI
2. fill in with Klenow + 4 dNTP
3. cut with Sal (TCGA)
4. isolate 1232 bp fragment



1. cut with XhoI (TCGA) and HpaI
2. gel purify



1 CTCGCACTCCCTCTGGCCGGCCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGCGCCACG6AACCCGCTCGATCTCGCCGCCAACTGGTAGAC
 100 ATG GAG ACC CCT GCC TGG CCC CGG GTC CCG CGC CCC GAG ACC GCC GTC GCT CGG AGC CTC CTG CTC GGC TGG GTC
 -32 Met Glu Thr Pro Ala Trp Pro Arg Val Pro Arg Pro Glu Thr Ala Val Ala Arg Thr Leu Leu Gly Trp Val
 175 TTC GCC CAG GTG GCC GGC GCT TCA GGC ACT ACA AAT ACT GTG GCA GCA TAT AAT TTA ACT TGG AAA TCA ACT AAT
 -7 Phe Ala Gln Val Ala Gly Ala Ser Gly Thr Thr Asn Thr Val Ala Ala Tyr Asn Leu Thr Trp Lys Ser Thr Asn
 250 TTC AAG ACA ATT TTG GAG TGG GAA CCC AAA CCC GTC AAT CAA GTC TAC ACT GTT CAA ATA AGC ACT AAG TCA GGA
 19 Phe Lys Thr Ile Leu Glu Trp Glu Pro Val Asn Gln Val Tyr Thr Val Gln Ile Ser Thr Lys Ser Gly
 325 GAT TGG AAA AGC AAA TGC TTT TAC ACA ACA GAC ACA GAG TGT GAC CTC ACC GAC GAG ATT GTG AAG GAT GTG AAG
 44 Asp Trp Lys Ser Lys Cys Phe Tyr Thr Asp Thr Glu Cys Asp Leu Thr Asp Glu Ile Val Lys Asp Val Lys
 400 CAG ACG TAC TTG GCA CGG GTC TTC TCC TAC CCG GCA GGG AAT GTG GAG AGC ACC GGT TCT GCT GGG GAG CCT CTG
 69 Gln Thr Tyr Leu Ala Arg Val Phe Ser Tyr Pro Ala Gln Asn Val Glu Ser Thr Gly Ser Ala Gly Glu Pro Leu
 475 TAT GAG AAC TCC CCA GAG TTC ACA CCT TAC CTG GAG ACA AAC CTC GGA CAG CCA ACA ATT CAG AGT TTT GAA CAG
 94 Tyr Glu Asn Ser Pro Glu Phe Thr Pro Tyr Leu Glu Thr Asn Leu Gly Gln Pro Thr Ile Gln Ser Phe Glu Gln
 550 GTG GGA ACA AAA GTG AAT GTG ACC GTC GAA GAT GAA CGG ACT TTA GTC AGA AGG AAC AAC ACT TTC CTA AGC CTC
 119 Val Gly Thr Val Asn Val Thr Val Glu Asp Glu Arg Thr Leu Val Arg Arg Asn Asn Thr Phe Leu Ser Leu
 625 CGG GAT GTT TTT GGC AAG GAC TTA ATT TAT ACA CTT TAT TAT TGG AAA TCT TCA AGT TCA GGA AAG AAA ACA GCC
 144 Arg Asp Val Phe Gly Lys Asp Leu Ile Tyr Thr Leu Tyr Trp Lys Ser Ser Ser Gly Lys Thr Ala
 700 AAA ACA AAC ACT AAT GAG TTT TTG ATT GAT GTG GAT AAA GGA GAA AAC TAC TGT TTC AGT GTT CAA GCA GTG ATT
 169 Lys Thr Asn Thr Asn Glu Phe Leu Ile Asp Val Asp Lys Gly Glu Asn Tyr Cys Phe Ser Val Gln Ala Val Ile
 775 CCC TCC CGA ACA GTT AAC CGG AAG AGT ACA GAC AGC AGC CCG GTC GAG TGT ATG GGC CAG GAG AAA GGG GAA TTC AGA
 174 Pro Ser Arg Thr Val Asn Arg Lys Ser Thr Asp Ser Pro Val Glu Cys Met Gly Gln Glu Lys Gly Glu Phe Arg
 850 GAA ATA TTC TAC ATC ATT GGA GCT GTG GTC ATC ATC CTT GTC ATC ATC CTG GCT ATA TCT CTA CAC
 219 Glu Ile Phe Tyr Ile Ile Gly Ala Val Val Phe Val Val Ile Ile Leu Val Ile Ile Leu Ala Ile Ser Leu His
 925 AAG TGT AGA AAG GCA GGA GTG GGG CAG AGC TGG AAG GAG AAC TCC CCA CTG AAT GTT TCA TAA AGGAAGCACTGTTGG
 244 Lys Cys Arg Lys Ala Gln Val Gln Ser Trp Lys Glu Asn Ser Pro Leu Asn Val Ser End
 1003 AGCTACTGCAAATGCTATATTGACTGTGACCGAGAACTTTAAGAGGATAGAATACATGGAAACGCAAATGAGTATTCGGAGCATGAAGACCCCTGGAG
 1103 TTCAAAAAACTTGTATATGACCTGTTATTACCATGGCATTCTGGTTGACATCAGCATTAGTCATTTGAAATGTAACGAATGGTACTACAACCAAT
 1203 TCCAGTTAATTTAACACCATGGCACCTTTGACATAACATGCTTGTAGATTATATTCCGCACTCAAGGAGTAACCAGGTCTCCAAGCAAAAA
 1303 CAAATGGGAAATGTCTAAAAAAATCCTGGGTGGACTTTGAAAAGCTT \rightarrow TTTTTTTTTTGAGACGGAGTCTGCTCTGTTGCCAGGCTGGA
 1403 GTGAGTAGCACGATCTGGCTCACTGCACCCCTCCGTCTCGGGTTCAAGCAATTGTCGCTCAGCCTCCGAGTAGCTGGATTACAGGTGCGCACT
 1503 ACCACACCAAGCTAATTTGTATTTTAGAGAGATGGGGTTCACCATCTGGCAGGCTGGCTTGAATTCCGACCTCAGTTGATCCACCCACCT
 1603 TGGCCTCCAAAGTGTAGTATTATGGCGTGAACCACCATGCCAGCCGAAAGCTT \rightarrow TGAGGGCTGACTTCATCCATGTAGGAAAGTAAATGGAA
 1703 GGAAATTGGGTGCTTTCTAGGACTTTCTAACATATGTCATAATATAGTGTGTTAGGTTCTTTTTTTTCAAGGAATACATTGGAAATTCAAAACAT
 1803 TGGCAAACCTTGATTAATGTGTTAAGTGCAGGAGACATTGGTATTCTGGCACCTTCTAACATGCTTACAATCTGCACTTAACTGACTTAAGTGGC
 1903 ATTAAACATTGAGAGCTAACTATTTTATAAGACTACTACAAACTACAGAGTTATGATTTAAGGTACTTAAAGCTTCTATGGTTGACATTGTAT
 2003 ATATAATTTTAAAAAGGTTTCTATATGGGGATTTCTATTATGTAGGTAATATTGTTCTATTGTATATTGAGATAATTATTAATACTTT
 2103 AAATAAAGGTGACTGGGAATTGTTA

FIG. 3a

FIG
3b

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FIG. 5

